

OIEPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/954,556

DATE: 10/09/2001
 TIME: 08:54:19

Input Set : A:\RTS-0250_Seq_ASCII.txt
 Output Set: N:\CRF3\10092001\I954556.raw

3 <110> APPLICANT: Brett P. Monia
 4 Susan M. Freier
 5 Scott Cooper
 7 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 2

EXPRESSION

9 <130> FILE REFERENCE: RTS-0250
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/954,556
 C--> 11 <141> CURRENT FILING DATE: 2001-09-14

11 <160> NUMBER OF SEQ ID NOS: 108

14 <210> SEQ ID NO: 1

15 <211> LENGTH: 20

16 <212> TYPE: DNA

17 <213> ORGANISM: Artificial Sequence

19 <220> FEATURE:

21 <223> OTHER INFORMATION: Antisense Oligonucleotide

23 <400> SEQUENCE: 1

24 tccgtcatcg ctctcaggg

27 <210> SEQ ID NO: 2

28 <211> LENGTH: 20

29 <212> TYPE: DNA

30 <213> ORGANISM: Artificial Sequence

32 <220> FEATURE:

34 <223> OTHER INFORMATION: Antisense Oligonucleotide

36 <400> SEQUENCE: 2

37 atgcattctg cccccaagga

40 <210> SEQ ID NO: 3

41 <211> LENGTH: 4268

42 <212> TYPE: DNA

43 <213> ORGANISM: Homo sapiens

45 <220> FEATURE:

47 <220> FEATURE:

48 <221> NAME/KEY: CDS

49 <222> LOCATION: (274)...(2739)

51 <400> SEQUENCE: 3

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54 tccatcccgga ccacgcggg gcgcggggac aacacaggtc gcggaggagc gttgccattc 120

56 aagtgactgc agcagcagcg gcagcgcttc ggttcctgag cccaccgcag gctgaaggca 180

58 ttgcgcgtag tccatgccc tagaggaagt gtgcagatgg gattaacgtc cacatggaga 240

60 tatggaagag gaccggggat tggatccgta acc atg gtc agc tgg ggt cgt ttc 294

61 Met Val Ser Trp Gly Arg Phe

62 1 5

64 atc tgc ctg gtc gtg gtc acc atg gca acc ttg tcc ctg gcc cgg ccc 342

65 Ile Cys Leu Val Val Val Thr Met Ala Thr Leu Ser Leu Ala Arg Pro

66 10 15 20

68 tcc ttc agt tta gtt gag gat acc aca tta gag cca gaa gag cca cca 390

69 Ser Phe Ser Leu Val Glu Asp Thr Thr Leu Glu Pro Glu Glu Pro Pro

70 25 30 35

72 acc aaa tac caa atc tct caa cca gaa gtg tac gtg gct gcg cca ggg 438

ENTERED

20

20

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73 Thr Lys Tyr Gln Ile Ser Gln Pro Glu Val Tyr Val Ala Ala Pro Gly
74 40 45 50 55
76 gag tcg cta gag gtg cgc tgc ctg ttg aaa gat gcc gcc gtg atc agt 486
77 Glu Ser Leu Glu Val Arg Cys Leu Leu Lys Asp Ala Ala Val Ile Ser
78 60 65 70
80 tgg act aag gat ggg gtg cac ttg ggg ccc aac aat agg aca gtg ctt 534
81 Trp Thr Lys Asp Gly Val His Leu Gly Pro Asn Asn Arg Thr Val Leu
82 75 80 85
84 att ggg gag tac ttg cag ata aag ggc gcc acg cct aga gac tcc ggc 582
85 Ile Gly Glu Tyr Leu Gln Ile Lys Gly Ala Thr Pro Arg Asp Ser Gly
86 90 95 100
88 ctc tat gct tgt act gcc agt agg act gta gac agt gaa act tgg tac 630
89 Leu Tyr Ala Cys Thr Ala Ser Arg Thr Val Asp Ser Glu Thr Trp Tyr
90 105 110 115
92 ttc atg gtg aat gtc aca gat gcc atc tca tcc gga gat gat gag gat 678
93 Phe Met Val Asn Val Thr Asp Ala Ile Ser Ser Gly Asp Asp Glu Asp
94 120 125 130 135
96 gac acc gat ggt gcg gaa gat ttt gtc agt gag aac agt aac aac aag 726
97 Asp Thr Asp Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn Asn Lys
98 140 145 150
100 aga gca cca tac tgg acc aac aca gaa aag atg gaa aag cgg ctc cat 774
101 Arg Ala Pro Tyr Trp Thr Asn Thr Glu Lys Met Glu Lys Arg Leu His
102 155 160 165
104 gct gtg cct gcg gcc aac act gtc aag ttt cgc tgc cca gcc ggg ggg 822
105 Ala Val Pro Ala Ala Asn Thr Val Lys Phe Arg Cys Pro Ala Gly Gly
106 170 175 180
108 aac cca atg cca acc atg cgg tgg ctg aaa aac ggg aag gag ttt aag 870
109 Asn Pro Met Pro Thr Met Arg Trp Leu Lys Asn Gly Lys Glu Phe Lys
110 185 190 195
112 cag gag cat cgc att gga ggc tac aag gta cga aac cag cac tgg agc 918
113 Gln Glu His Arg Ile Gly Gly Tyr Lys Val Arg Asn Gln His Trp Ser
114 200 205 210 215
116 ctc att atg gaa agt gtg gtc cca tct gac aag gga aat tat acc tgt 966
117 Leu Ile Met Glu Ser Val Val Pro Ser Asp Lys Gly Asn Tyr Thr Cys
118 220 225 230
120 gtg gtg gag aat gaa tac ggg tcc atc aat cac acg tac cac ctg gat 1014
121 Val Val Glu Asn Glu Tyr Gly Ser Ile Asn His Thr Tyr His Leu Asp
122 235 240 245
124 gtt gtg gag cga tcg cct cac cgg ccc atc ctc caa gcc gga ctg ccg 1062
125 Val Val Glu Arg Ser Pro His Arg Pro Ile Leu Gln Ala Gly Leu Pro
126 250 255 260
128 gca aat gcc tcc aca gtg gtc gga gga gac gta gag ttt gtc tgc aag 1110
129 Ala Asn Ala Ser Thr Val Val Gly Gly Asp Val Glu Phe Val Cys Lys
130 265 270 275
132 gtt tac agt gat gcc cag ccc cac atc cag tgg atc aag cac gtg gaa 1158
133 Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Ile Lys His Val Glu
134 280 285 290 295
136 aag aac ggc agt aaa tac ggg ccc gac ggg ctg ccc tac ctc aag gtt 1206
137 Lys Asn Gly Ser Lys Tyr Gly Pro Asp Gly Leu Pro Tyr Leu Lys Val

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138		300		305		310		
140	ctc aag gcc gcc ggt gtt aac acc acg gac aaa gag att gag gtt ctc							1254
141	Leu Lys Ala Ala Gly Val Asn Thr Thr Asp Lys Glu Ile Glu Val Leu							
142		315		320		325		
144	tat att cgg aat gta act ttt gag gac gct ggg gaa tat acg tgc ttg							1302
145	Tyr Ile Arg Asn Val Thr Phe Glu Asp Ala Gly Glu Tyr Thr Cys Leu							
146		330		335		340		
148	gcg ggt aat tct att ggg ata tcc ttt cac tct gca tgg ttg aca gtt							1350
149	Ala Gly Asn Ser Ile Gly Ile Ser Phe His Ser Ala Trp Leu Thr Val							
150		345		350		355		
152	ctg cca gcg cct gga aga gaa aag gag att aca gct tcc cca gac tac							1398
153	Leu Pro Ala Pro Gly Arg Glu Lys Glu Ile Thr Ala Ser Pro Asp Tyr							
154	360		365		370		375	
156	ctg gag ata gcc att tac tgc ata ggg gtc ttc tta atc gcc tgt atg							1446
157	Leu Glu Ile Ala Ile Tyr Cys Ile Gly Val Phe Leu Ile Ala Cys Met							
158		380		385		390		
160	gtg gta aca gtc atc ctg tgc cga atg aag aac acg acc aag aag cca							1494
161	Val Val Thr Val Ile Leu Cys Arg Met Lys Asn Thr Thr Lys Lys Pro							
162		395		400		405		
164	gac ttc agc agc cag ccg gct gtg cac aag ctg acc aaa cgt atc ccc							1542
165	Asp Phe Ser Ser Gln Pro Ala Val His Lys Leu Thr Lys Arg Ile Pro							
166		410		415		420		
168	ctg cgg aga cag gta aca gtt tcg gct gag tcc agc tcc tcc atg aac							1590
169	Leu Arg Arg Gln Val Thr Val Ser Ala Glu Ser Ser Ser Ser Met Asn							
170		425		430		435		
172	tcc aac acc ccg ctg gtg agg ata aca aca cgc ctc tct tca acg gca							1638
173	Ser Asn Thr Pro Leu Val Arg Ile Thr Thr Arg Leu Ser Ser Thr Ala							
174	440		445		450		455	
176	gac acc ccc atg ctg gca ggg gtc tcc gag tat gaa ctt cca gag gac							1686
177	Asp Thr Pro Met Leu Ala Gly Val Ser Glu Tyr Glu Leu Pro Glu Asp							
178		460		465		470		
180	cca aaa tgg gag ttt cca aga gat aag ctg aca ctg ggc aag ccc ctg							1734
181	Pro Lys Trp Glu Phe Pro Arg Asp Lys Leu Thr Leu Gly Lys Pro Leu							
182		475		480		485		
184	gga gaa ggt tgc ttt ggg caa gtg gtc atg gcg gaa gca gtg gga att							1782
185	Gly Glu Gly Cys Phe Gly Gln Val Val Met Ala Glu Ala Val Gly Ile							
186		490		495		500		
188	gac aaa gac aag ccc aag gag gcg gtc acc gtg gcc gtg aag atg ttg							1830
189	Asp Lys Asp Lys Pro Lys Glu Ala Val Thr Val Ala Val Lys Met Leu							
190		505		510		515		
192	aaa gat gat gcc aca gag aaa gac ctt tct gat ctg gtg tca gag atg							1878
193	Lys Asp Asp Ala Thr Glu Lys Asp Leu Ser Asp Leu Val Ser Glu Met							
194	520		525		530		535	
196	gag atg atg aag atg att ggg aaa cac aag aat atc ata aat ctt ctt							1926
197	Glu Met Met Lys Met Ile Gly Lys His Lys Asn Ile Ile Asn Leu Leu							
198		540		545		550		
200	gga gcc tgc aca cag gat ggg cct ctc tat gtc ata gtt gag tat gcc							1974
201	Gly Ala Cys Thr Gln Asp Gly Pro Leu Tyr Val Ile Val Glu Tyr Ala							
202		555		560		565		

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204	tct	aaa	ggc	aac	ctc	cga	gaa	tac	ctc	cga	gcc	cgg	agg	cca	ccc	ggg	2022
205	Ser	Lys	Gly	Asn	Leu	Arg	Glu	Tyr	Leu	Arg	Ala	Arg	Arg	Pro	Pro	Gly	
206			570					575					580				
208	atg	gag	tac	tcc	tat	gac	att	aac	cgt	gtt	cct	gag	gag	cag	atg	acc	2070
209	Met	Glu	Tyr	Ser	Tyr	Asp	Ile	Asn	Arg	Val	Pro	Glu	Glu	Gln	Met	Thr	
210		585					590				595						
212	ttc	aag	gac	ttg	gtg	tca	tgc	acc	tac	cag	ctg	gcc	aga	ggc	atg	gag	2118
213	Phe	Lys	Asp	Leu	Val	Ser	Cys	Thr	Tyr	Gln	Leu	Ala	Arg	Gly	Met	Glu	
214	600					605					610				615		
216	tac	ttg	gct	tcc	caa	aaa	tgt	att	cat	cga	gat	tta	gca	gcc	aga	aat	2166
217	Tyr	Leu	Ala	Ser	Gln	Lys	Cys	Ile	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	
218				620						625					630		
220	gtt	ttg	gta	aca	gaa	aac	aat	gtg	atg	aaa	ata	gca	gac	ttt	gga	ctc	2214
221	Val	Leu	Val	Thr	Glu	Asn	Asn	Val	Met	Lys	Ile	Ala	Asp	Phe	Gly	Leu	
222			635					640						645			
224	gcc	aga	gat	atc	aac	aat	ata	gac	tat	tac	aaa	aag	acc	acc	aat	ggg	2262
225	Ala	Arg	Asp	Ile	Asn	Asn	Ile	Asp	Tyr	Tyr	Lys	Lys	Thr	Thr	Asn	Gly	
226			650				655						660				
228	cgg	ctt	cca	gtc	aag	tgg	atg	gct	cca	gaa	gcc	ctg	ttt	gat	aga	gta	2310
229	Arg	Leu	Pro	Val	Lys	Trp	Met	Ala	Pro	Glu	Ala	Leu	Phe	Asp	Arg	Val	
230		665				670					675						
232	tac	act	cat	cag	agt	gat	gtc	tgg	tcc	ttc	ggg	gtg	tta	atg	tgg	gag	2358
233	Tyr	Thr	His	Gln	Ser	Asp	Val	Trp	Ser	Phe	Gly	Val	Leu	Met	Trp	Glu	
234	680				685					690					695		
236	atc	ttc	act	tta	ggg	ggc	tcg	ccc	tac	cca	ggg	att	ccc	gtg	gag	gaa	2406
237	Ile	Phe	Thr	Leu	Gly	Gly	Ser	Pro	Tyr	Pro	Gly	Ile	Pro	Val	Glu	Glu	
238			700					705						710			
240	ctt	ttt	aag	ctg	ctg	aag	gaa	gga	cac	aga	atg	gat	aag	cca	gcc	aac	2454
241	Leu	Phe	Lys	Leu	Leu	Lys	Glu	Gly	His	Arg	Met	Asp	Lys	Pro	Ala	Asn	
242			715					720					725				
244	tgc	acc	aac	gaa	ctg	tac	atg	atg	atg	agg	gac	tgt	tgg	cat	gca	gtg	2502
245	Cys	Thr	Asn	Glu	Leu	Tyr	Met	Met	Met	Arg	Asp	Cys	Trp	His	Ala	Val	
246			730				735						740				
248	ccc	tcc	cag	aga	cca	acg	ttc	aag	cag	ttg	gta	gaa	gac	ttg	gat	cga	2550
249	Pro	Ser	Gln	Arg	Pro	Thr	Phe	Lys	Gln	Leu	Val	Glu	Asp	Leu	Asp	Arg	
250		745				750					755						
252	att	ctc	act	ctc	aca	acc	aat	gag	gaa	tac	ttg	gac	ctc	agc	caa	cct	2598
253	Ile	Leu	Thr	Leu	Thr	Thr	Asn	Glu	Glu	Tyr	Leu	Asp	Leu	Ser	Gln	Pro	
254	760				765					770				775			
256	ctc	gaa	cag	tat	tca	cct	agt	tac	cct	gac	aca	aga	agt	tct	tgt	tct	2646
257	Leu	Glu	Gln	Tyr	Ser	Pro	Ser	Tyr	Pro	Asp	Thr	Arg	Ser	Ser	Cys	Ser	
258			780					785						790			
260	tca	gga	gat	gat	tct	gtt	ttt	tct	cca	gac	ccc	atg	cct	tac	gaa	cca	2694
261	Ser	Gly	Asp	Asp	Ser	Val	Phe	Ser	Pro	Asp	Pro	Met	Pro	Tyr	Glu	Pro	
262			795					800					805				
264	tgc	ctt	cct	cag	tat	cca	cac	ata	aac	ggc	agt	gtt	aaa	aca	tga		2739
265	Cys	Leu	Pro	Gln	Tyr	Pro	His	Ile	Asn	Gly	Ser	Val	Lys	Thr			
266			810				815					820					
268	atgactgtgt	ctgcctgtcc	ccaaacagga	cagcactggg	aacctagcta	cactgagcag											2799

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270 ggagaccatg cctcccagag cttgttgtct ccacttgtat atatggatca gaggagtaaa 2859
272 taattggaaa agtaatcagc atatgtgtaa agatttatac agttgaaaac ttgtaatctt 2919
274 ccccaggagg agaagaaggt ttctggagca gtggactgcc acaagccacc atgtaacccc 2979
276 tctcacctgc cgtgcgttct ggctgtggac cagtaggact caaggtggac gtgcgttctg 3039
278 ccttccttgt taattttgta ataattggag aagatttatg tcagcacaca cttacagagc 3099
280 acaaatgcag tatataggtg ctggatgtat gtaaataatat tcaaattatg tataaatata 3159
282 tattatataat ttacaaggag ttattttttg tattgatttt aaatggatgt cccaatgcac 3219
284 ctgaaaaatt ggtctctctt tttttaatag ctatttgcta aatgctgttc ttacacataa 3279
286 tttcttaatt ttcaccgagc agaggtggaa aaatactttt gctttcaggg aaaatggtat 3339
288 aacgttaatt tattaataaa ttggtaatat acaaaaacaat taatcattta tagttttttt 3399
290 tgtaatttaa gtggcatttc tatgcaggca gcacagcaga ctagttaatc tattgcttgg 3459
292 acttaactag ttatcagatc ctttgaaaag agaataatga caatatatga ctaatttggg 3519
294 gaaaatgaag ttttgattta tttgtgttta aatgctgctg tcagacgatt gttcttagac 3579
296 ctctaaatg ccccatatta aaagaactca ttcataggaa ggtgtttcat tttggtgtgc 3639
298 aaccctgtca ttacgtcaac gcaacgtcta actggacttc ccaagataaa tggtagcagc 3699
300 gtctctttaa aagatgcctt aatccattcc ttgaggacag accttagttg aaatgatagc 3759
302 agaatgtgct tctctctggc agctggcctt ctgcttctga gttgcacatt aatcagatta 3819
304 gcctgattct cttcagtga ttttgataat ggcttccaga ctctttgctg tggagacgcc 3879
306 tgtaggagc ttcaagtccc atcatagaaa attgaaacac agagttgttc tgctgatagt 3939
308 tttggggata cgtccatctt ttttaaggat tgctttcatc taattctggc aggacctcac 3999
310 caaaagatcc agcctcatc ctacatcaga caaaatatcg ccgttggtcc ttctgtacta 4059
312 aagtattgtg ttttgctttg gaaacacca ctcactttgc aatagccgtg caagatgaat 4119
314 gcagattaca ctgatcttat gtgttacaaa attggagaaa gtatttaata aaacctgtta 4179
316 atttttatac tgacaataaa aatgtttcta cagatattaa tgttaacaag acaaaataaa 4239
318 tgtcacgcaa cttaaaaaaa aaaaaaaaaa 4268
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322 <211> LENGTH: 22
323 <212> TYPE: DNA
324 <213> ORGANISM: Artificial Sequence
326 <220> FEATURE:
328 <223> OTHER INFORMATION: PCR Primer
330 <400> SEQUENCE: 4
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334 <210> SEQ ID NO: 5
335 <211> LENGTH: 19
336 <212> TYPE: DNA
337 <213> ORGANISM: Artificial Sequence
339 <220> FEATURE:
341 <223> OTHER INFORMATION: PCR Primer
343 <400> SEQUENCE: 5
344 tgggtcggga tggagaaag 19
347 <210> SEQ ID NO: 6
348 <211> LENGTH: 20
349 <212> TYPE: DNA
350 <213> ORGANISM: Artificial Sequence
352 <220> FEATURE:
354 <223> OTHER INFORMATION: PCR Probe
356 <400> SEQUENCE: 6
357 cccacaaccc cgggctcgtc 20

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1191 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1192 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1193 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1603 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1604 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1605 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:5150 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:5413 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29